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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,651A

DATE: 10/18/2002

TIME: 10:31:00

Input Set : A:\59150-8009.US00.txt

Output Set: N:\CRF4\10182002\I857651A.raw

ENTERED

4 <110> APPLICANT: Seki, Tatsuji
5 Fujiyama, Kazuhito
6 Yoshida, Toshiomi
8 <120> TITLE OF INVENTION: A Method for Manufacturing Glycoproteins
9 Having Human-type Glycosylation
12 <130> FILE REFERENCE: 9150-0009.10
14 <140> CURRENT APPLICATION NUMBER: US 09/857,651A
15 <141> CURRENT FILING DATE: 1999-12-08
17 <150> PRIOR APPLICATION NUMBER: PCT/JP99/06881
18 <151> PRIOR FILING DATE: 1999-12-08
20 <150> PRIOR APPLICATION NUMBER: JP 10-350584
21 <151> PRIOR FILING DATE: 1998-12-09
23 <160> NUMBER OF SEQ ID NOS: 6
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 31
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: primer hGT-5Eco
35 <400> SEQUENCE: 1
36 aaagaattcg cgatgccagg cgcgcgtccc t
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 28
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: primer hGT-2Sal
46 <400> SEQUENCE: 2
47 tcgacgcgcaa aacctgtgtc agctgatg
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 29
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: primer hGT-7Spe
57 <400> SEQUENCE: 3
58 acgggactcc tcaggggcga tgatcataa
60 <210> SEQ ID NO: 4
61 <211> LENGTH: 27
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:

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66 <223> OTHER INFORMATION: primer hGT-6Spe
68 <400> SEQUENCE: 4
69 aaagactagtg ggccccatgc tgattga 27
71 <210> SEQ ID NO: 5
72 <211> LENGTH: 1158
73 <212> TYPE: DNA
74 <213> ORGANISM: Homo sapiens
76 <220> FEATURE:
77 <221> NAME/KEY: CDS
78 <222> LOCATION: (1)...(1155)
80 <400> SEQUENCE: 5
81 atg cca ggc gcg tcc cta cag cgg gcc tgc cgc ctg ctc gtg gcc gtc 48
82 Met Pro Gly Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val
83 1 5 10 15
85 tgc gct ctg cac ctt ggc gtc acc ctc gtt tac tac ctg gct ggc cgc 96
86 Cys Ala Leu His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg
87 20 25 30
89 gac ctg agc cgc ctg ccc caa ctg gtc gga gtc tcc aca ccg ctg cag 144
90 Asp Leu Ser Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln
91 35 40 45
93 ggc ggc tcg aac agt gcc gcc gcc atc ggg cag tcc tcc ggg gag ctc 192
94 Gly Gly Ser Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu
95 50 55 60
97 cgg acc gga ggg gcc cgg ccg ccg cct cct cta ggc gcc tcc tcc cag 240
98 Arg Thr Gly Gly Ala Arg Pro Pro Pro Pro Leu Gly Ala Ser Ser Gln
99 65 70 75 80
101 ccg cgc ccg ggt ggc gac tcc agc cca gtc gtg gat tct ggc cct ggc 288
102 Pro Arg Pro Gly Gly Asp Ser Ser Pro Val Val Asp Ser Gly Pro Gly
103 85 90 95
105 ccc gct agc aac ttg acc tcg gtc cca gtg ccc cac acc acc gca ctg 336
106 Pro Ala Ser Asn Leu Thr Ser Val Pro Val Pro His Thr Thr Ala Leu
107 100 105 110
109 tcg ctg ccc gcc tgc cct gag gag tcc ccg cta cta gtg ggc ccc atg 384
110 Ser Leu Pro Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly Pro Met
111 115 120 125
113 ctg att gag ttt aac atg cct gtg gac ctg gag ctc gtg gca aag cag 432
114 Leu Ile Glu Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala Lys Gln
115 130 135 140
117 aac cca aat gtg aag atg ggc ggc cgc tat gcc ccc agg gac tgc gtc 480
118 Asn Pro Asn Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp Cys Val
119 145 150 155 160
121 tct cct cac aag gtg gcc atc atc att cca ttc cgc aac cgg cag gag 528
122 Ser Pro His Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg Gln Glu
123 165 170 175
125 cac ctc aag tac tgg cta tat tat ttg cac cca gtc ctg cag cgc cag 576
126 His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln Arg Gln
127 180 185 190
129 cag ctg gac tat ggc atc tat gtt atc aac cag gcg gga gac act ata 624
130 Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp Thr Ile

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131          195          200          205
133 ttc aat cgt gct aag ctc ctc aat gtt ggc ttt caa gaa gcc ttg aag      672
134 Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala Leu Lys
135      210      215      220
137 gac tat gac tac acc tgc ttt gtg ttt agt gac gtg gac ctc att cca      720
138 Asp Tyr Asp Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu Ile Pro
139 225      230      235      240
141 atg aat gac cat aat gcg tac agg tgt ttt tca cag cca cgg cac att      768
142 Met Asn Asp His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg His Ile
143      245      250      255
145 tcc gtt gca atg gat aag ttt gga ttc agc cta cct tat gtt cag tat      816
146 Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr
147      260      265      270
149 ttt gga ggt gtc tct gct cta agt aaa caa cag ttt cta acc atc aat      864
150 Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn
151      275      280      285
153 gga ttt cct aat aat tat tgg ggc tgg gga gga gaa gat gat gac att      912
154 Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp Ile
155      290      295      300
157 ttt aac aga tta gtt ttt aga ggc atg tct ata tct cgc cca aat gct      960
158 Phe Asn Arg Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala
159 305      310      315      320
161 gtg gtc ggg agg tgt cgc atg atc cgc cac tca aga gac aag aaa aat      1008
162 Val Val Gly Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn
163      325      330      335
165 gaa ccc aat cct cag agg ttt gac cga att gca cac aca aag gag aca      1056
166 Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr
167      340      345      350
169 atg ctc tct gat ggt ttg aac tca ctc acc tac cag gtg ctg gat gta      1104
170 Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val
171      355      360      365
173 cag aga tac cca ttg tat acc caa atc aca gtg gac atc ggg aca ccg      1152
174 Gln Arg Tyr Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly Thr Pro
175      370      375      380
177 agc tag      1158
178 Ser
179 385
182 <210> SEQ ID NO: 6
183 <211> LENGTH: 385
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
187 <400> SEQUENCE: 6
188 Met Pro Gly Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val
189 1      5      10      15
190 Cys Ala Leu His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg
191      20      25      30
192 Asp Leu Ser Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln
193      35      40      45
194 Gly Gly Ser Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu

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195      50      55      60
196 Arg Thr Gly Gly Ala Arg Pro Pro Pro Pro Leu Gly Ala Ser Ser Gln
197 65      70      75      80
198 Pro Arg Pro Gly Gly Asp Ser Ser Pro Val Val Asp Ser Gly Pro Gly
199      85      90      95
200 Pro Ala Ser Asn Leu Thr Ser Val Pro Val Pro His Thr Thr Ala Leu
201      100      105      110
202 Ser Leu Pro Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly Pro Met
203      115      120      125
204 Leu Ile Glu Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala Lys Gln
205      130      135      140
206 Asn Pro Asn Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp Cys Val
207 145      150      155      160
208 Ser Pro His Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg Gln Glu
209      165      170      175
210 His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln Arg Gln
211      180      185      190
212 Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp Thr Ile
213      195      200      205
214 Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala Leu Lys
215      210      215      220
216 Asp Tyr Asp Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu Ile Pro
217 225      230      235      240
218 Met Asn Asp His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg His Ile
219      245      250      255
220 Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr
221      260      265      270
222 Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn
223      275      280      285
224 Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp Ile
225      290      295      300
226 Phe Asn Arg Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala
227 305      310      315      320
228 Val Val Gly Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn
229      325      330      335
230 Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr
231      340      345      350
232 Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val
233      355      360      365
234 Gln Arg Tyr Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly Thr Pro
235      370      375      380
236 Ser
237 385

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VERIFICATION SUMMARY

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